



1

SEQUENCE LISTING

<110> Kock, Michael
Hoeger, Thomas
Kroeger, Burkhard
Otterbach, Bernd
Lubisch, Wilfried
Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586

<141> 1999-06-04

<150> PCT/EP99/03889

<151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)...(1715)

<223> product is Poly ADP Ribose Polymerase; from brain tissue

<400> 1

cc atg gcg gcg cgg cgg cga cgg agc acc ggc ggc ggc agg gcg aga 47
Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
1 5 10 15

gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95
Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
20 25 30

gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143
Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
35 40 45

aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
50 55 60

gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala
65 70 75

cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287
Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
80 85 90 95

Seul
Ch

2

tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc	335
Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu	
100 105 110	
cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat	383
Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp	
115 120 125	
gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa	431
Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys	
130 135 140	
atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc	479
Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala	
145 150 155	
aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg	527
Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp	
160 165 170 175	
gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta	575
Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu	
180 185 190	
cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa	623
Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys	
195 200 205	
gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt	671
Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu	
210 215 220	
cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa	719
Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu	
225 230 235	
gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg	767
Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly	
240 245 250 255	
aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag	815
Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys	
260 265 270	
att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa	863
Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu	
275 280 285	
gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt	911
Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg	
290 295 300	
act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa	959
Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln	
305 310 315	
tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa	1007
Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys	
320 325 330 335	

aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac	1055
Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn	
340 345 350	
cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa	1103
Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys	
355 360 365	
gtg att tcc cag tac cta caa tct acc cat gct ccc aca cac agc gac	1151
Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp	
370 375 380	
tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag	1199
Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu	
385 390 395	
aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat	1247
Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His	
400 405 410 415	
ggg tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga	1295
Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg	
420 425 430	
att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga	1343
Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly	
435 440 445	
atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc	1391
Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala	
450 455 460	
tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta	1439
Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu	
465 470 475	
ggg cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg	1487
Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu	
480 485 490 495	
ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt	1535
Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser	
500 505 510	
tct gcc cac ttc gtc acc ctg aat ggg agt aca gtg cca tta gga cca	1583
Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro	
515 520 525	
gca agt gac aca gga att ctg aat cca gat ggt tat acc ctc aac tac	1631
Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr	
530 535 540	
aat gaa tat att gta tat aac ccc aac cag gtc cgt atg cgg tac ctt	1679
Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu	
545 550 555	
tta aag gtt cag ttt aat ttc ctt cag ctg tgg tga atgttgatat	1725
Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp	
560 565 570	

4

taaataaacc agagatctga tcttcaagca agaaaataag cagtgttgta cttgtgaatt 1785

ttgtgatatt ttatgtaata aaaactgtac aggtctaaaa aaaaaaaaaa aaaaaaaaaa 1843

<210> 2

<211> 570

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
1 5 10 15

Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
20 25 30

Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
35 40 45

Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
50 55 60

Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala Pro
65 70 75 80

Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
85 90 95

Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
100 105 110

Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
115 120 125

Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
130 135 140

Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
145 150 155 160

Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
165 170 175

Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
180 185 190

Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu
195 200 205

Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
210 215 220

Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
225 230 235 240

Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
245 250 255

Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
 260 265 270
 Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
 275 280 285
 Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
 290 295 300
 Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
 305 310 315 320
 Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
 325 330 335
 Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
 340 345 350
 His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
 355 360 365
 Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
 370 375 380
 Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
 385 390 395 400
 Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
 405 410 415
 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
 420 425 430
 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
 435 440 445
 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
 450 455 460
 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
 465 470 475 480
 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
 485 490 495
 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
 500 505 510
 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
 515 520 525
 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
 530 535 540
 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
 545 550 555 560
 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
 565 570

<210> 3
 <211> 2265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242)...(1843)
 <223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 3

tgggactggt cgcctgactc ggccctgcccc agcctctgct tcacccact ggtggccaaa	60
tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc	120
tctccctaat tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag	180
gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc	240
c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag	286
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu	
1 5 10 15	
aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc	334
Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser	
20 25 30	
acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc	382
Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg	
35 40 45	
gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat	430
Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr	
50 55 60	
gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac	478
Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn	
65 70 75	
aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc	526
Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe	
80 85 90 95	
acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca aag	574
Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys	
100 105 110	
atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag aag	622
Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys	
115 120 125	
aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac ttt	670
Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe	
130 135 140	
gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag gat	718
Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp	

145	150	155	
gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg act			766
Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr			
160	165	170	175
gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag aag			814
Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys			
	180	185	190
ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg gcc			862
Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala			
	195	200	205
ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc aag			910
Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys			
	210	215	220
caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag gcc			958
Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala			
	225	230	235
ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc tca			1006
Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser			
	240	245	255
cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc ccg			1054
His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro			
	260	265	270
ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg ctg			1102
Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu			
	275	280	285
gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct gag			1150
Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu			
	290	295	300
cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac tac			1198
Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr			
	305	310	315
cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct gag			1246
Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu			
	320	325	330
tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac agg			1294
Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg			
	340	345	350
tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag gaa			1342
Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu			
	355	360	365
gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg tgg			1390
Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp			
	370	375	380
cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg ctc			1438

8

His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu	
385 390 395	
cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac ttt	1486
Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe	
400 405 410 415	
gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag tgt	1534
Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys	
420 425 430	
ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg ggc	1582
Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly	
435 440 445	
aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca cct	1630
Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro	
450 455 460	
cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat ccg	1678
Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro	
465 470 475	
acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg ccc	1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro	
480 485 490 495	
cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc tcc	1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser	
500 505 510	
cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc tac	1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr	
515 520 525	
ctg ctg gag gtc cac ctc tga gtgccccgcc tgtcccccg ggtcctgcaa	1873
Leu Leu Glu Val His Leu	
530	
ggctggactg tgatcttcaa tcatactgcc catctctggt acccctatat cactcctttt	1933
tttcaagaat acaatacggt gttgttaact atagtcacca tgctgtacaa gatccctgaa	1993
cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc	2053
cagcccatgg taaccagcat ttgactcttt acttgataaa gggcagcttt tataggttcc	2113
acatgtaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat	2173
aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaaa	2233
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	2265

<210> 4

<211> 533

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys
 1 5 10 15
 Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 20 25 30
 Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val
 35 40 45
 Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
 50 55 60
 Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn
 65 70 75 80
 Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr
 85 90 95
 Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile
 100 105 110
 Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys
 115 120 125
 Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val
 130 135 140
 Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu
 145 150 155 160
 Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val
 165 170 175
 Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu
 180 185 190
 Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu
 195 200 205
 Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln
 210 215 220
 Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu
 225 230 235 240
 Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His
 245 250 255
 Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro
 260 265 270
 Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val
 275 280 285
 Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln
 290 295 300

10

Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 305 310 315 320
 Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
 325 330 335
 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
 340 345 350
 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
 370 375 380
 Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415
 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
 420 425 430
 Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
 435 440 445
 Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460
 Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
 465 470 475 480
 Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
 485 490 495
 Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
 500 505 510
 Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
 515 520 525
 Leu Glu Val His Leu
 530

<210> 5

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (221)...(1843)

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 5

tgggactggt cgcctgactc ggccctgcccc agcctctgct tcacccact ggtggccaaa

60

tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc	120
tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag	180
gcgcacacaaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc	235
Met Ser Leu Leu Phe	
1 5	
ttg gcc atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct	283
Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro	
10 15 20	
gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc	331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg	
25 30 35	
tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc	379
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile	
40 45 50	
cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg	427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val	
55 60 65	
tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac	475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn	
70 75 80 85	
aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc	523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe	
90 95 100	
ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca	571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser	
105 110 115	
aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag	619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu	
120 125 130	
aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac	667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His	
135 140 145	
ttt gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag	715
Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu	
150 155 160 165	
gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg	763
Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg	
170 175 180	
act gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag	811
Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln	
185 190 195	
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg	859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met	
200 205 210	

12

gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc	907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser	
215 220 225	
aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag	955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu	
230 235 240 245	
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc	1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser	
250 255 260	
tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc	1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro	
265 270 275	
ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg	1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu	
280 285 290	
ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct	1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser	
295 300 305	
gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac	1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp	
310 315 320 325	
tac cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct	1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro	
330 335 340	
gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac	1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His	
345 350 355	
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag	1339
Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu	
360 365 370	
gaa gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg	1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu	
375 380 385	
tgg cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg	1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly	
390 395 400 405	
ctc cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac	1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr	
410 415 420	
ttt gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag	1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys	
425 430 435	
tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg	1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu	
440 445 450	

13

```

ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca      1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro
   455                               460                               465

cct cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat      1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp
  470                               475                               480                               485

ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg      1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val
                               490                               495                               500

ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc      1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe
                               505                               510                               515

tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc      1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg
   520                               525                               530

tac ctg ctg gag gtc cac ctc tga gtgccccgcc tgtcccccg ggtcctgcaa      1873
Tyr Leu Leu Glu Val His Leu
   535                               540

ggctggactg tgatcttcaa tcatcctgcc catctctggt acccctatat cactcctttt      1933

tttcaagaat acaatacgtt gttgttaact atagtcacca tgctgtacaa gatccctgaa      1993

cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc      2053

cagcccatgg taaccagcat ttgactcttt acttgtataa gggcagcttt tataggttcc      2113

acatgtaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat      2173

aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaaa      2233

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                                  2265

```

<210> 6

<211> 540

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
  1                               5                               10                               15

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
                20                               25                               30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
    35                               40                               45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
    50                               55                               60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr

```

14

65	70					75					80				
Asn Ile Glu Asn Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln	85					90					95				
Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly	100					105					110				
Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala	115					120					125				
Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp	130					135					140				
Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile	145					150					155				
Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp	165					170					175				
Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu	180					185					190				
Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met	195					200					205				
Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro	210					215					220				
Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu	225					230					235				
Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser	245					250					255				
Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe	260					265					270				
Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala	275					280					285				
Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala	290					295					300				
Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His	305					310					315				
Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu	325					330					335				
Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln	340					345					350				
Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val	355					360					365				
Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly	370					375					380				

15

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
385 390 395 400

Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
405 410 415

Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
420 425 430

Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
435 440 445

Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
450 455 460

Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
465 470 475 480

His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
485 490 495

Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
500 505 510

Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
515 520 525

Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu
530 535 540

<210> 7

<211> 1740

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (112) ... (1710)

<400> 7

cccggctttc actttttctg ctgcctcggg gaacacctcg agccaactgc ttcctaactc 60

agggtgggca gaactgacgg gatctaagct tctgcatctc tgaggagaac c atg gct 117
Met Ala
1

cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
5 10 15

caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc 213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
20 25 30

aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
35 40 45 50

16

cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt	309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys	
55 60 65	
acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att	357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile	
70 75 80	
atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg	405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp	
85 90 95	
ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
100 105 110	
ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
115 120 125 130	
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
135 140 145	
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
150 155 160	
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
165 170 175	
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
180 185 190	
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
195 200 205 210	
gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
215 220 225	
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
230 235 240	
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	
245 250 255	
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc	933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser	
260 265 270	
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac	981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp	
275 280 285 290	

atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag	1029
Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu	
295 300 305	
aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc	1077
Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu	
310 315 320	
agg tgc cag ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca	1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala	
325 330 335	
ata cag acc tac ctg aaa cag act ggc aac agc tac agg tgc cca aac	1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn	
340 345 350	
ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc	1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe	
355 360 365 370	
cag gcc cac tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc	1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr	
375 380 385	
aat gtg gcc gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg	1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met	
390 395 400	
cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag	1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu	
405 410 415	
aac agc aag tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac	1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His	
420 425 430	
cag gtg ggc tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac	1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His	
435 440 445 450	
cac atc acc atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt	1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe	
455 460 465	
gac agc gtc atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac	1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp	
470 475 480	
att gaa ctt gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg	1605
Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro	
485 490 495	
cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa	1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu	
500 505 510	
tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag	1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu	
515 520 525 530	

18

att cac ctc taagctgctt gccctcccta ggtccaagcc
Ile His Leu

1740

<210> 8
<211> 533
<212> PRT
<213> Mus musculus

<400> 8

Met	Ala	Pro	Lys	Arg	Lys	Ala	Ser	Val	Gln	Thr	Glu	Gly	Ser	Lys	Lys	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Glu	Glu	Glu	Asp	Ser	Phe	Arg	Ser	Thr	Ala	Glu	20	25	30	
Ala	Leu	Arg	Ala	Ala	Pro	Ala	Asp	Asn	Arg	Val	Ile	Arg	Val	Asp	Pro	35	40	45	
Ser	Cys	Pro	Phe	Ser	Arg	Asn	Pro	Gly	Ile	Gln	Val	His	Glu	Asp	Tyr	50	55	60	
Asp	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Gly	Asn	Asn	Asn	Asn	Lys	Phe	65	70	75	80
Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Glu	Gly	Ser	Arg	Phe	Phe	Cys	Trp	Asn	85	90	95	
Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Met	Asn	His	Phe	100	105	110	
Thr	Cys	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Lys	Lys	Lys	Phe	Trp	Glu	115	120	125	
Lys	Thr	Lys	Asn	Lys	Trp	Glu	Glu	Arg	Asp	Arg	Phe	Val	Ala	Gln	Pro	130	135	140	
Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu	145	150	155	160
Ala	Val	Val	Lys	Ala	Leu	Ser	Pro	Gln	Val	Asp	Ser	Gly	Pro	Val	Arg	165	170	175	
Thr	Val	Val	Lys	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	180	185	190	
Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	195	200	205	
Asn	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	210	215	220	
Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	225	230	235	240
Asn	Pro	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	245	250	255	

19

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile
 260 265 270
 Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
 275 280 285
 Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu
 290 295 300
 Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 305 310 315 320
 Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
 325 330 335
 Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
 340 345 350
 Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
 370 375 380
 Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415
 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
 420 425 430
 Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
 435 440 445
 Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460
 Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
 465 470 475 480
 Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
 485 490 495
 Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln
 500 505 510
 Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu
 515 520 525
 Leu Glu Ile His Leu
 530

<210> 9

<211> 1587

<212> DNA

<213> Mus musculus

20

<220>

<221> CDS

<222> (1)...(1584)

<400> 9

atg gct cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag	48
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys	
1 5 10 15	
cag cga caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag	96
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
20 25 30	
gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc	144
Ala Leu Arg Ala Ala Pro Ala Asn Arg Val Ile Arg Val Asp Pro	
35 40 45	
tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat	192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
50 55 60	
gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc	240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	
65 70 75 80	
tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat	288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	
85 90 95	
cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc	336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	
100 105 110	
acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	
115 120 125	
aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc	432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
130 135 140	
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
145 150 155 160	
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
165 170 175	
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
180 185 190	
aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
195 200 205	
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc	672

21

Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	
210					215						220					
gag	gcc	ttg	gaa	gct	cta	gag	gag	gcc	atg	aaa	aac	ccc	aca	ggg	gat	720
Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp	
225					230					235					240	
ggc	cag	agc	ctg	gaa	gag	ctc	tcc	tcc	tgc	ttc	tac	act	gtc	atc	cca	768
Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro	
				245					250					255		
cac	aac	ttc	ggc	cgc	agc	cga	ccc	ccg	ccc	atc	aac	tcc	cct	gat	gtg	816
His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val	
			260					265					270			
ctt	cag	gcc	aag	aag	gac	atg	ctg	ctg	gtg	cta	gcg	gac	atc	gag	ttg	864
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	
		275					280						285			
gcg	cag	acc	ttg	cag	gca	gcc	cct	ggg	gag	gag	gag	gag	aaa	gtg	gaa	912
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu	
		290				295					300					
gag	gtg	cca	cac	cca	ctg	gat	cga	gac	tac	cag	ctc	ctc	agg	tgc	cag	960
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln	
305					310					315					320	
ctt	caa	ctg	ctg	gac	tcc	ggg	gag	tcc	gag	tac	aag	gca	ata	cag	acc	1008
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr	
				325					330					335		
tac	ctg	aaa	cag	act	ggc	aac	agc	tac	agg	tgc	cca	aac	ctg	cgg	cat	1056
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	
			340					345					350			
gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	cag	gcc	cac	1104
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	
		355					360					365				
tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	aat	gtg	gcc	1152
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	
	370					375					380					
gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	cca	cac	tgc	1200
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	
385					390					395					400	
ggt	ggt	cgt	gtt	ggc	aag	ggt	att	tat	ttt	gcc	tct	gag	aac	agc	aag	1248
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	
				405					410					415		
tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	cag	gtg	ggc	1296
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	
			420					425					430			
tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	cac	atc	acc	1344
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	
		435				440							445			

22

atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt gac agc gtc 1392
 Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
 450 455 460

atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac att gaa ctt 1440
 Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
 465 470 475 480

gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg cct gtg cag 1488
 Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa tac ctc ata 1536
 Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag att cac ctc 1584
 Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

taa 1587

<210> 10
 <211> 528
 <212> PRT
 <213> Mus musculus

<400> 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
 145 150 155 160

23

Ala	Val	Val	Lys	Val	Asp	Ser	Gly	Pro	Val	Arg	Thr	Val	Val	Lys	Pro	165	170	175
Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	Thr	Asn	Ile	Phe	Ser	180	185	190
Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	Asn	Leu	Asp	Val	Lys	195	200	205
Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	210	215	220
Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp	225	230	235
Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro	245	250	255
His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val	260	265	270
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	275	280	285
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu	290	295	300
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln	305	310	315
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr	325	330	335
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	340	345	350
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	355	360	365
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	370	375	380
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	385	390	395
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	405	410	415
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	420	425	430
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	435	440	445
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val	450	455	460
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu	465	470	475

24

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

<210> 11
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (2)...(6), (9)...(11)
 <223> any amino acid; residues 3 to 6 may be present or absent

<220>
 <221> VARIANT
 <222> (7)
 <223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr
 1 5 10 15

Phe Ala

<210> 12
 <211> 25
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (1), (14)
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>
 <221> VARIANT
 <222> (2), (7), (9)...(13), (16)...(18)
 <223> may be any amino acid; 10-13 may be present or absent

<220>
 <221> VARIANT
 <222> (6)
 <223> amino acid residue 6 is either Ile or Val

25

<400> 12

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa
 1 5 10 15

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
 20 25

<210> 13

<211> 49

<212> PRT

<213> artificial sequence

<220>

<223> NAD+ binding domain

<220>

<221> VARIANT

<222> (6), (16), (29)

<223> Ser or Thr

<220>

<221> VARIANT

<222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)

<223> may be any amino acid; residues 25-28 may be present or absent

<220>

<221> VARIANT

<222> 21

<223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
 35 40 45

Tyr

<210> 14

<211> 22

<212> PRT

<213> artificial sequence

<220>

<223> leucine zipper motif

<220>

<221> VARIANT

<222> (1)

<223> Leu or Val

26

<220>

<221> VARIANT

<222> (2)...(7), (9)...(14), (16)...(21)

<223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
 20

<210> 15

<211> 37

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 1

<220>

<221> VARIANT

<222> (21)

<223> Asp or Glu

<220>

<221> VARIANT

<222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)

<223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
 1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Trp Gly Arg Val Gly
 35

<210> 16

<211> 29

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 2

<220>

<221> VARIANT

<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)

<223> may be any amino acid

<400> 16

27

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
 1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
 20 25

<210> 17
 <211> 44
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 3

<220>
 <221> VARIANT
 <222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)
 <223> may be any amino acid

<220>
 <221> VARIANT
 <222> (4)
 <223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
 20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
 35 40

<210> 18
 <211> 15
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 4

<220>
 <221> VARIANT
 <222> (4), (8), (11)...(13)
 <223> may be any amino acid

<400> 18

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro
 1 5 10 15

<210> 19
 <211> 17
 <212> PRT

28

<213> artificial sequence

<220>

<223> part-sequence motif 5

<220>

<221> VARIANT

<222> (2)...(4), (6)...(7), (9), (13), (15)...(16)

<223> may be any amino acid

<400> 19

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
 1 5 10 15

Leu

<210> 20

<211> 11

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 6

<220>

<221> VARIANT

<222> (2)...(4), (6)

<223> may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1 5 10

<210> 21

<211> 28

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 7

<220>

<221> VARIANT

<222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)

<223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
 20 25

29

<210> 22
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 8

<220>
 <221> VARIANT
 <222> (2)
 <223> Tyr or Phe

<220>
 <221> VARIANT
 <222> (3)...(4), (6)...(8), (10)...(13)
 <223> may be any amino acid

<400> 22

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Tyr Leu Leu
 1 5 10 15

<210> 23
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 23

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
 1 5 10 15

Leu Asn Glu Ser
 20

<210> 24
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 24

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg
 1 5 10 15

Asn Leu His Cys
 20

30

<210> 25
 <211> 21
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 1 5 10 15

Ala Glu Ala Leu Lys
 20

<210> 26
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
 1 5 10 15

Glu Ala Leu Lys
 20

<210> 27
 <211> 19
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 1 5 10 15

Ala Leu Lys

<210> 28
 <211> 19
 <212> PRT
 <213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 1 5 10 15

31

Ala Met Lys

<210> 29
 <211> 7
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (2)...(4)
 <223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly
 1 5

<210> 30
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PARP zinc finger sequence motif

<220>
 <221> VARIANT
 <222> (2)...(3), (5)...(34), (36)...(37)
 <223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa His Xaa Xaa Cys
 35

<210> 31
 <211> 10
 <212> PRT
 <213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 1 5 10

<210> 32

32

<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10

39

<210> 33
<211> 13
<212> PRT
<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10